

Table S1. Allelic profiles of invasive serotype 35B isolates from 1994 to 2014

ST (n)	<i>aroE</i>	<i>gdh</i>	<i>gki</i>	<i>recP</i>	<i>spi</i>	<i>xpt</i>	<i>ddl</i>
558 (54)	18	12	4	44	14	77	97
10493 (2)	8	12	4	44	14	77	97
10063 (1)	18	12	429	44	14	77	97
11866 (1)	18	12	4	15	14	77	97
4679 (1)	1	12	4	44	14	77	97
SLV558 (1)	18	12	4	5	14	77	97
SLV558 (1)	18	9	4	44	14	77	97
SLV558 (1)	18	12	4	16	14	77	97
SLV558 (1)	18	12	4	44	511	77	97
SLV558 (1)	18	519	4	44	14	77	97
DLV558 (1)	18	12	1	44	14	389	97
156 (8)	7	11	10	1	6	8	1
SLV558 (1)	7	11	10	1	402	8	1
452 (3)	7	9	19	1	14	48	14
198 (1)	8	13	4	8	6	22	34

Each line represents a sequence type (ST). STs with a white background represent a variant of ST558 or ST156. Alleles in red represent a difference from the founder ST.

SLV: single-locus variant; DLV: double-locus variant.

Table S2. Demographic characteristics of patients with invasive and noninvasive serotype 35B isolates from 2011 to 2014.

	Invasive (n=38)	Noninvasive ^a (n=48)	<i>p</i>
Age, months (IQR)	15.6 (6.9-53.2)	15.7 (10.3-21.3)	0.87
No. of males (%)	24 (63.2)	33 (68.8)	0.65
Race/ethnicity (%)			
White	15 (39.5)	30/44 (68.2)	0.01
Black	14 (36.8)	6/44 (13.6)	0.02
Hispanic	6 (15.8)	7/44 (15.9)	1
Other	3 (7.9)	1/44 (2.3)	
Comorbidity (%)	21 (55.3)	7 (14.6)	<0.001
PCV13, at least one dose (%) ^b	25/32 (78.1)	45/47 (95.7)	0.03

^a Race/ethnicity data was not available for 4 patients with noninvasive isolates.

^b Immunization status was not available for 6 patients with invasive isolates and in 1 patient with a noninvasive isolate.

IQR: interquartile range.

Table S3. Allelic profiles of non-invasive serotype 35B isolates from 2011 to 2014

ST (n)	<i>aroE</i>	<i>gdh</i>	<i>gki</i>	<i>recP</i>	<i>spi</i>	<i>xpt</i>	<i>ddl</i>
558 (33)	18	12	4	44	14	77	97
10493 (1)	8	12	4	44	14	77	97
10063 (1)	18	12	429	44	14	77	97
6961 (1)	18	12	313	44	14	77	97
SLV558 (1)	378	12	4	44	14	77	97
DLV558 (1)	351	12	4	44	23	77	97
156 (8)	7	11	10	1	6	8	1
11584 (1)	7	12	10	1	6	8	1
2414 (1)	2	8	36	12	17	21	14

Each line represents a sequence type (ST). STs with a white background represent a variant of ST558 or ST156. Alleles in red represent a difference from the founder ST.

SLV: single-locus variant; DLV: double-locus variant.

Table S4. Antimicrobial susceptibility of invasive and noninvasive serotype 35B isolates from 2011 to 2014.

	Invasive (n=38)	Noninvasive (n=48)	<i>p</i>
Antibiotic MIC, median (IQR)			
Penicillin	1 (0.5-1.25)	1 (0.5-1.37)	0.3
Ceftriaxone	0.25 (0.25-0.5)	0.5 (0.25-0.5)	0.1
Nonsusceptible isolates (%)			
Penicillin (≥ 0.12 $\mu\text{g/ml}$)	34 (89.5)	48 (100)	0.03
Ceftriaxone (≥ 1 $\mu\text{g/ml}$)	3 (7.9)	9 (18.8)	0.2
Resistant isolates (%)			
Erythromycin	26 (68.4)	34 (70.8)	0.8
Clindamycin	1 (2.6)	2 (4.2)	1
TMP-SMX	14 (36.8)	13 (27.1)	
Multidrug resistant isolates (%)	12 (31.6)	15 (31.3)	1

IQR: interquartile range; MIC: minimum inhibitory concentration; TMP-SMX: trimethoprim-sulfamethoxazole.

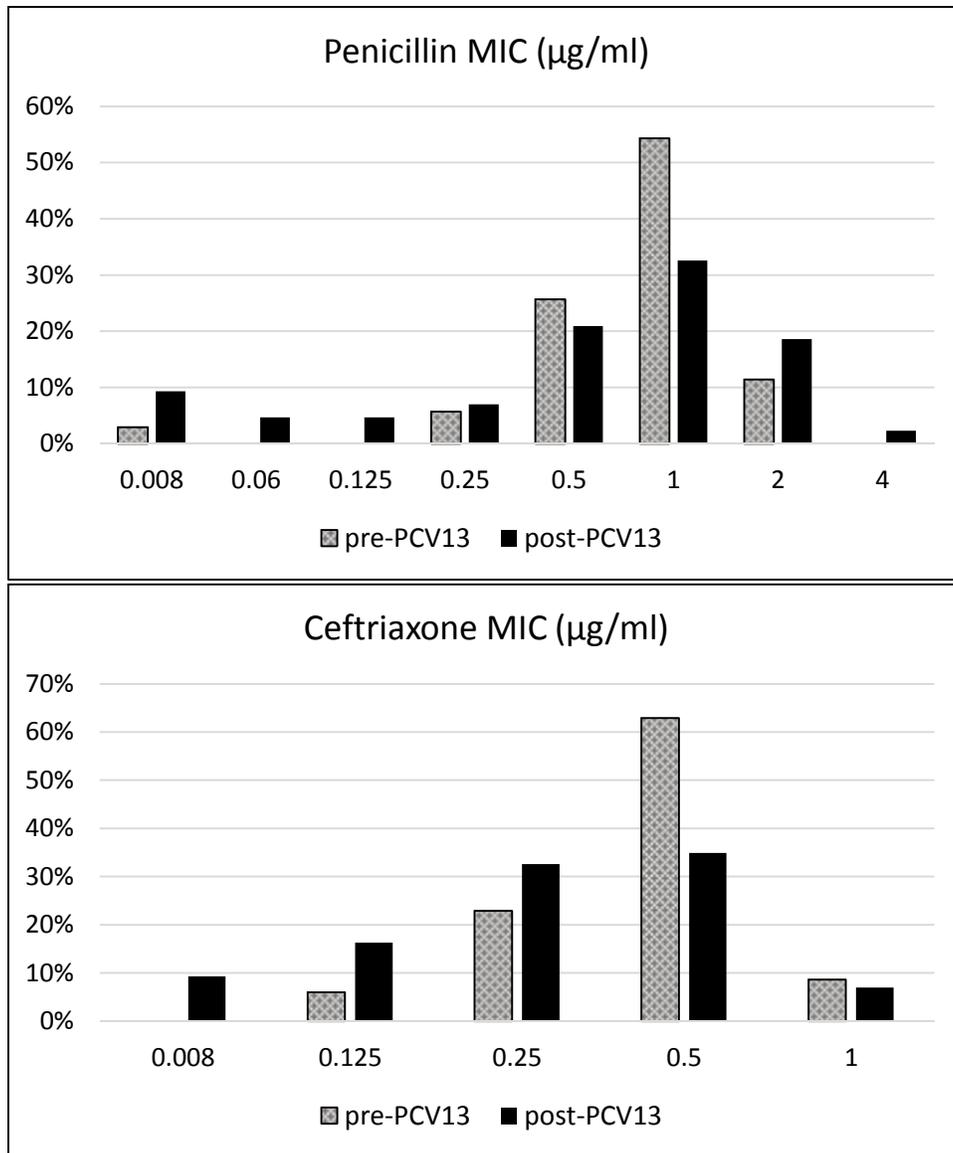


Fig S1. Percentage of serotype 35B isolates by penicillin and ceftriaxone minimum inhibitory concentration (MIC) and vaccine era.

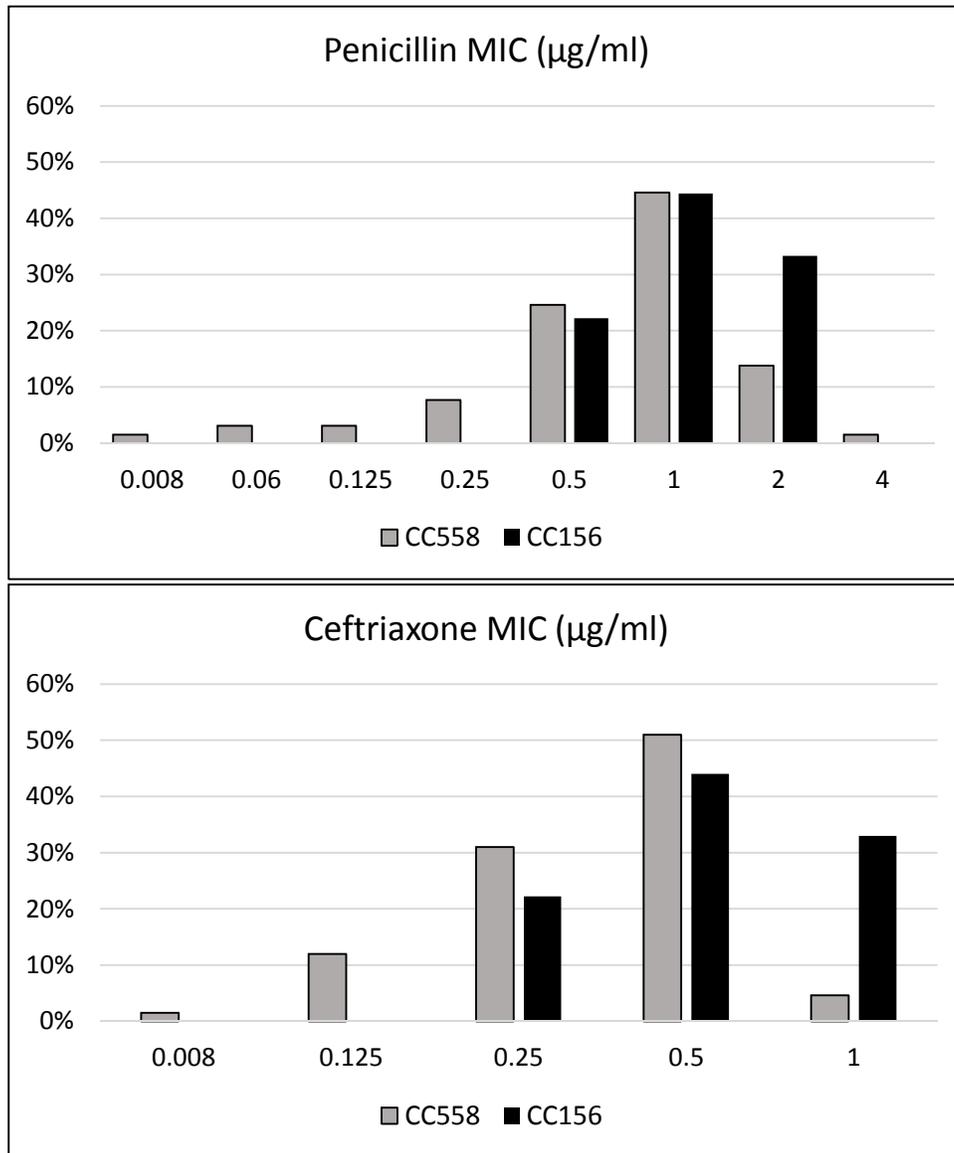


Fig S2. Percentage of serotype 35B isolates by penicillin and ceftriaxone minimum inhibitory concentration (MIC) and clonal complex (CC).